

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/768,996
Source: 1 FWO
Date Processed by STIC: 10/25/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Raw Sequence Listing Error Summary


ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10768,996

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) 1-3 contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
  Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 10/25/2004

PATENT APPLICATION: US/10/768,996

TIME: 14:42:06

Input Set : A:\Untitled.ST25.txt

Output Set: N:\CRF4\10252004\J768996.raw

3 <110> APPLICANT: Srivastava, Suresh C.
 4 Sit, Kwok-Hung
 5 Bajpai, Satya P.
 7 <120> TITLE OF INVENTION: Novel Oligonucleotides and Related Compounds
 9 <130> FILE REFERENCE: CHMG-10
 11 <140> CURRENT APPLICATION NUMBER: 10/768,996
 12 <141> CURRENT FILING DATE: 2004-01-30
 14 <150> PRIOR APPLICATION NUMBER: 60/525691
 15 <151> PRIOR FILING DATE: 2003-11-28
 17 <160> NUMBER OF SEQ ID NOS: 10
 19 <170> SOFTWARE: PatentIn version 3.3
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 5
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: misc_feature
 29 <222> LOCATION: (3)..(3)
 30 <223> OTHER INFORMATION: n represents one or more nucleotides which can be the same or
 31 different from each other.
 33 <400> SEQUENCE: 1

W--> 34 gcgc

5

37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 5
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Homo sapiens
 43 <220> FEATURE:
 44 <221> NAME/KEY: misc_feature
 45 <222> LOCATION: (3)..(3)
 46 <223> OTHER INFORMATION: n represents one or more nucleotides which can be the same or
 47 different from each other.
 50 <400> SEQUENCE: 2

W--> 51 gcgc

5

54 <210> SEQ ID NO: 3
 55 <211> LENGTH: 5
 56 <212> TYPE: DNA
 57 <213> ORGANISM: Artificial
 59 <220> FEATURE:
 60 <223> OTHER INFORMATION: Artificial sequence
 63 <220> FEATURE:
 64 <221> NAME/KEY: misc_feature
 65 <222> LOCATION: (3)..(4) (3) "n" is only at location 3
 66 <223> OTHER INFORMATION: n represents one or more nucleotides which can be the same

or

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67 different as each other.

69 <400> SEQUENCE: 3

W--> 70 **cgncgc** 5

73 <210> SEQ ID NO: 4

74 <211> LENGTH: 6

75 <212> TYPE: DNA

76 <213> ORGANISM: Artificial

78 <220> FEATURE:

79 <223> OTHER INFORMATION: Artificial sequence

82 <220> FEATURE:

83 <221> NAME/KEY: misc_feature

84 <222> LOCATION: (3)..(4)

85 <223> OTHER INFORMATION: Each n represents any nucleotide, which can be the same or

86 different from other nucleotides that are labeled "n"

88 <400> SEQUENCE: 4

W--> 89 **gcnnngc** 6

92 <210> SEQ ID NO: 5

93 <211> LENGTH: 8

94 <212> TYPE: DNA

95 <213> ORGANISM: Artificial

97 <220> FEATURE:

98 <223> OTHER INFORMATION: Artificial sequence

101 <220> FEATURE:

102 <221> NAME/KEY: misc_feature

103 <222> LOCATION: (3)..(8)(6)←

104 <223> OTHER INFORMATION: Each n represents any nucleotide, which can be the same or

105 different from other nucleotides that are labeled "n"

107 <400> SEQUENCE: 5

W--> 108 **gcnnnnngc** 8

111 <210> SEQ ID NO: 6

112 <211> LENGTH: 13

113 <212> TYPE: DNA

114 <213> ORGANISM: Artificial

116 <220> FEATURE:

117 <223> OTHER INFORMATION: Artificial sequence

120 <220> FEATURE:

121 <221> NAME/KEY: misc_feature

122 <222> LOCATION: (3)..(11)

123 <223> OTHER INFORMATION: Each n represents any nucleotide, which can be the same or

124 different from other nucleotides that are labeled "n"

126 <400> SEQUENCE: 6

W--> 127 **gcnnnnnnnnn gc** 13

130 <210> SEQ ID NO: 7

131 <211> LENGTH: 6

132 <212> TYPE: DNA

133 <213> ORGANISM: Artificial

135 <220> FEATURE:

136 <223> OTHER INFORMATION: Artificial sequence

139 <220> FEATURE:

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Input Set : A:\Untitled.ST25.txt

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140 <221> NAME/KEY: modified_base
141 <222> LOCATION: (1)..(1)
142 <223> OTHER INFORMATION: n represents 2'-deoxy, 2',2'-difluorocytidine
145 <400> SEQUENCE: 7

W--> 146 nggacg 6
149 <210> SEQ ID NO: 8
150 <211> LENGTH: 9
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Artificial sequence
158 <220> FEATURE:
159 <221> NAME/KEY: modified_base
160 <222> LOCATION: (1)..(1)
161 <223> OTHER INFORMATION: n represents 2'-deoxy, 2',2'-difluorocytidine
165 <400> SEQUENCE: 8

W--> 166 ngtggaacg 9
169 <210> SEQ ID NO: 9
170 <211> LENGTH: 13
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Artificial sequence
178 <220> FEATURE:
179 <221> NAME/KEY: modified_base
180 <222> LOCATION: (1)..(1)
181 <223> OTHER INFORMATION: n represents 2'-deoxy, 2',2'-difluorocytidine
184 <400> SEQUENCE: 9

W--> 185 nggacgtgga acg 13
188 <210> SEQ ID NO: 10
189 <211> LENGTH: 13
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Artificial sequence
197 <220> FEATURE:
198 <221> NAME/KEY: modified_base
199 <222> LOCATION: (1)..(1)
200 <223> OTHER INFORMATION: n represents 2'-deoxy, 2',2' difluorocytidine
204 <400> SEQUENCE: 10

W--> 205 nggagctgga acg 13

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/768,996

DATE: 10/25/2004
TIME: 14:42:07

Input Set : A:\Untitled.ST25.txt
Output Set: N:\CRF4\10252004\J768996.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 3
Seq#:2; N Pos. 3
Seq#:3; N Pos. 3
Seq#:4; N Pos. 3,4
Seq#:5; N Pos. 3,4,5,6
Seq#:6; N Pos. 3,4,5,6,7,8,9,10,11
Seq#:7; N Pos. 1
Seq#:8; N Pos. 1
Seq#:9; N Pos. 1
Seq#:10; N Pos. 1

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10

VERIFICATION SUMMARY

DATE: 10/25/2004

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Input Set : A:\Untitled.ST25.txt

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L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0